The MaRS (Matrix of RNA-Seq) Project

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Recent years have seen a dramatic increase in the amount of genomic and transcriptomic data produced by laboratories around the world. The aim of the MaRS research program is to collect and to allow the comparison of these data. MaRS is focused on the RNA-Seq method, which reflects the expression of the genes in a specific condition.

RNA-Seq method is used in a wide variety of applications like identifying disease-related genes, analysing the effects of drugs on tissues or providing insight into disease pathways. The RNA-Seq is widely used to identify gene expression patterns associated with tumor formation. MaRS represents a fantastic tool for the discovery and the validation of Biomarkers.

27000 Human RNA-Seq profiles are selected for the project. In collaboration with the CINES, all these data are collected and computed with a single method to allow their compilation in one matrix: MaRS. It represents a huge amount of data and requires the use of High performance computing (HPC) on the cluster Occigen (CINES): 120 To of compressed data downloaded and 1.2 million hours/core consumed.

Many challenges were encountered and solved during the project:
- the download of the very large amount of data
- the installation and the settings of the software’s in the cluster
- the optimization of the compiler and the packages
- the constraints in jobs duration and jobs limitations.

Next? The Exploration of MaRS! Implementation of an advanced search tool to query the matrix in order to highlight biomarkers.

Extend work to other species: Mouse.

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